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8 418 2 US-09-134-001C-1723 Sequence 418 2 US-09-328-352-4525 Sequence US-09-758-759-121 Sequence US-09-949-016-9739 Sequence US-09-949-016-9739 Sequence US-09-949-016-9739 Sequence US-09-930-930-972-420-2 Sequence US-09-902-540-15774 Sequence	8 441 2 US-09-052-778-14 Sequence 8 443 2 US-09-949-016-6420 Sequence 8 443 2 US-09-830-230A-21 Sequence 8 444 2 US-09-371-608-8 Sequence	.8 444 2 US-09-695-950-8 Sequence 8 444 2 US-09-696-1417-8 Sequence 8 444 2 US-09-696-1417-8 Sequence 8 444 2 US-08-696-344-8 Sequence	.8 444 2 US-10-043-452A-8 Sequence .8 447 2 US-09-605-703B-1482 Sequence	.8 449 2 US-09-270-767-57465 Sequence .8 455 2 US-09-134-000C-6074 Sequence	.8 458 2 US-09-407-062-9 .8 478 2 US-09-489-039A-7300 Sequence .8 490 2 US-09-902-540-10306 Sequence	8 493 2 US-08-657-749D-2 Sequence 8 495 2 US-09-991-552-20 Sequence	18 498 2 US-09-232-468A-24 Sequence 8 408 2 US-09-232-468A-24 Sequence 8 408 2 US-09-784-54 Semience	8 510 2 US-10-104-047-2339 Sequence	.8 533 2 US-09-605-703B-1480 Sequence .8 541 2 US-09-328-352-7237 Sequence	.8 546 2 US-09-489-039A-9631 Sequence .8 566 2 US-09-491-522-7 Sequence	.8 566 2 US-09-949-016-7010 Sequence .8 568 2 US-09-218-702-4 Sequence	.8 591 2 US-09-252-991A-26716 Sequence .8 608 2 US-09-949-016-8981 Sequence	8 608 2 US-09-949-016-11561 Sequence	.8 615 1 US-08-083-508A-1/ Sequence .8 615 1 US-08-023-610-17 Sequence .8 615 1 US-08-065A-17 Sequence	.8 615 1 US-08-362-240A-17 Sequence	8 635 2 US-09-341-833A-6 Sequence	8 635 2 US-09-341-833A-9 Sequence 9,	8 651 2 US-09-248-796A-18051 Sequence 18051,	.8 668 2 US-09-252-991A-26712 Sequence 2	.8 668 2 US-09-538-092-599 Sequence 3	.8 677 2 US-09-341-833A-8 Sequence E	.8 876 1 US-08-717-515-4 Sequence	.8 911 2 US-08-461-562B-2 Sequence 2.8 924 2 US-09-489-039A-8842 Sequence E.	.8 1039 2 US-09-328-352-5474 Sequence 5	. 1084 1 US-08-717-515-6 Sequence	.8 1092 2 US-09-252-991A-28476 Sequence 2	.8 1098 2 US-10-104-047-2475 Sequence 2	.8 1170 1 US-08-476-0628-42 Sequence	.8 1170 4 PCT-US96-01314-42 Sequence 4	.8 1227 2 US-09-688-188B-105 Sequence 1	.8 1227 2 US-09-291-417D-105 Sequence 1 .8 1247 2 US-09-134-000C-4968 Sequence 4	.8 1276 1 US-08-717-515-8 Sequence	.8 1407 2 US-09-328-352-7885 Sequence .8 1747 2 US-09-902-540-14765 Sequence
395 2 US-09-134-001C-3723 Sequence 418 2 US-09-328-322-4525 Sequence 420 2 US-09-328-322-4525 Sequence 428 2 US-09-949-016-9739 Sequence 429 2 US-09-949-016-9739 Sequence 430 2 US-09-902-540-15774 Sequence 4312 2 US-09-902-540-15774 Sequence	2.8 441 2 US-09-052-778-14 Sequence 2.8 443 2 US-09-949-016-6420 Sequence 2.8 444 2 US-09-830-230A-21 Sequence 2.8 444 2 US-09-830-230A-21 Sequence	2.8 444 2 US-09-695-950-8 Sequence 2.8 444 2 US-09-696-147-8 Sequence 2.8 444 2 US-09-696-147-8 Sequence 2.8 1RS-08-68-68-8 Sequence 2.8 1RS-08-68-8 Sequence 2.8 1RS-08-68-88-88-88-88-88-88-88-88-88-88-88-88	2.8 444 2 US-10-043-452A-8 Sequence 2.8 447 2 US-09-605-703B-1482 Sequence	2.8 449 2 US-09-270-767-57465 Sequence 2.8 455 2 US-09-134-000C-6074 Sequence	2.8 458 2 US-09-407-0828 2.8 478 2 US-09-489-039A-7300 Sequence 2.8 490 2 US-09-2540-10306 Sequence	2.8 493 2 US-08-657-749D-2 Sequence	2.8 498 2 US-02-32-468A-24 Sequence 2 4 498 2 US-02-32-468A-24 Sequence 2 8 498 2 US-0784-984R-54 Sequence	2.8 510 2 US-09-540-236-2597 Sequence 2.8 511 2 US-10-104-047-2339 Sequence	2.8 533 2 US-09-605-703B-1480 Sequence 2.8 541 2 US-09-328-352-7237 Sequence	2.8 546 2 US-09-489-039A-9631 Sequence 2.8 566 2 US-09-491-522-7 Sequence	2.8 566 2 US-09-949-016-7010 Sequence 2.8 568 2 US-09-218-702-4 Sequence	2.8 591 2 US-09-252-991A-26716 Sequence 2.8 608 2 US-09-949-016-8981 Sequence	2.8 608 2 US-09-949-016-11561 Sequence	2.8 615 1 US-08-083-508A-1/ Sequence 2.8 615 1 US-08-023-610-17 Sequence 2.8 615 1 US-08-288-065A-17 Sequence	2.8 615 1 US-08-362-240A-17 Sequence	2.8 635 2 US-09-341-833A-6 Sequence	2.8 635 2 US-09-341-833A-9 Sequence 9,	2.8 651 2 US-09-248-796A-18051 Sequence 18051,	2.8 668 2 US-09-252-991A-26712 Sequence 2	2.8 668 2 US-09-538-092-599 Sequence 5 2.8 673 2 US-09-252-991A-23922 Sequence 2	2.8 677 2 US-09-341-833A-8 Sequence 8	2.8 876 1 US-08-717-515-4 Sequence	2.8 911 2 US-08-461-562B-2 2.8 924 2 US-09-489-039A-8842 Sequence E	2.8 1039 2 US-09-328-352-5474 Sequence 5	2.8 1084 1 US-08-717-515-6 Sequence	2.8 1092 2 US-09-252-991A-28476 Sequence 2	2.8 1098 2 US-10-104-047-2475 Sequence 2	2.8 1170 1 US-08-476-062A-42 Sequence 4	2.8 1170 4 PCT-US96-01314-42 Sequence 4	2.8 1227 2 US-09-688-188B-105 Sequence 1	2.8 1227 2 US-09-291-417D-105 Sequence 1 2.8 1247 2 US-09-134-000C-4968 Sequence 4	2.8 1276 1 US-08-717-515-8 Sequence	2.8 1407 2 US-09-328-352-7885 Sequence 2.8 1747 2 US-09-902-540-14765 Sequence 2.9 1747 2 Equation 2.25.2325.3

1488 73 2.8 542 2 US-09-164-671-3 Sequence 3, Appli 1489 73 2.8 542 2 US-09-182-113-3 Sequence 3, Appli 1490 73 2.8 542 2 US-09-182-113-3 Sequence 3, Appli 1491 73 2.8 546 2 US-09-552-991A-31673 Sequence 3, Appli 1492 73 2.8 554 1 US-08-687-852-5 Sequence 5, Appli 1494 73 2.8 554 1 US-08-687-852-5 Sequence 5, Appli 1495 73 2.8 572 2 US-09-489-019A-9902 Sequence 5, Appli 1496 73 2.8 572 2 US-09-489-019A-9902 Sequence 61.6 Appli 1497 73 2.8 572 2 US-05-656-640A-4 Sequence 61.6 Appli 1497 73 2.8 573 2 US-09-556-640A-4 Sequence 61.6 Appli 1498 73 2.8 625 2 US-09-889-019A-256396 Sequence 12568, Appli 1499 73 2.8 730 2 US-09-489-019A-12568 Sequence 12568, Appli 1500 73 2.8 750 2 US-09-889-019A-12568 Sequence 12568, Appli 1500 73 2.8 750 2 US-09-581-110-4010 Sequence 4010, Appli 1500 73 2.8 750 2 US-09-581-110-4010	an a	Qy 142 DGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEODLPVNIKFIIEGMERA 201 Db 64 DGWTTNPFELTEVDGKLYGRGADKGPVLAWINAVSAFRALEODLPVNIKFIIEGMERS 123 Cy 202 GSVALEELVEKEKDRFFSGYDYLVISDNLMISQRKPAITYGTRGAPVNYKCRDODFH 261 Db 124 GSEGLDDLLDERKONFLADVPCISDNYMIGKRRCLTYGTRGAPYGVECSSKDLH 183 Cy 262 SGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVDLTEEBINTYKAIHLDLEEYR 321 Db 124 GSEGLDDLLHERWADLCHLLSILVDGTVDSTOVPLTEEBINTYKAIHLDLEEYR 321 Cy 262 SGTFGGILHEPMADLVALLGSLVDSSGHILVPGTVDEDVPLTEEBINTYKAIHLDLEEYR 243 Cy 322 NSSRVEKELPD-TKEBILMHLWRYPSLSHGIRGARPDEPOTKTVIPGKVIGKFSIRLVPH 380 Cy 324 KDIGWEQLPHNGDKTRLLQARWRYPELSHGIRGARYBCAKTVIPKKVIGKFSIRLVPH 303 Cy 334 MAVSAVEKQVTRHLEDVFSKRNSSNKAVVSMTLGILHPWIANIDDTQYLAAKRAIRTYFGT 440 Ch 1
Sequence 1, Appli Sequence 12282, A Sequence 9, Appli Sequence 21335, A Sequence 21335, A Sequence 7, Appli Sequence 30, Appl Sequence 8, Appli Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl	Sequence 2509, Appleagemence 2, Applia Sequence 2, Applia Sequence 2, Applia Sequence 1, Applia Sequence 1, Applia Sequence 1, Applia Sequence 1329, Applacemence 1329, Applacemence 24, Applia Sequence 15988, A Sequence 4, Applia Sequence 15988, A Sequence 15988, A Sequence 1538, Applacemence 25, Applia Sequence 26, Applia Sequence 20, Applia Se	Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 12816, A Sequence 4170, Ap Sequence 4170, Ap Sequence 21701, A Sequence 2, Appli Sequence 2, Appli Sequence 36, Appl Sequence 36, Appl Sequence 36, Appl Sequence 39, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli
US-08-215-709-1 US-09-489-039A-12282 US-09-206-800-9 US-09-252-991A-21335 US-09-751-389-7 US-09-751-389-7 US-08-702-357A-30 US-09-751-389-8 US-08-702-357A-30 US-09-751-389-8 US-08-702-357A-30 US-08-702-357A-30 US-09-791-389-8 US-08-79-98-453A-13 US-09-791-98-453A-13 US-09-791-98-453A-841	US-09-10-104-09-103-103-103-103-103-103-103-103-103-103	US-08-723-142A-20 US-09-528-764A-20 US-09-528-764A-20 US-09-902-540-12816 US-09-328-325-4470 US-09-328-325-4470 US-09-328-325-4470 US-09-328-325-921A-26701 US-09-225-991A-26701 US-09-107-433-4028 US-09-107-433-4028 US-09-107-433-4028 US-09-107-433-6 US-09-419-362-39 US-09-419-362-39 US-09-419-36-39 US-09-419-36-39 US-09-419-36-39 US-09-419-36-39 US-09-419-36-39 US-09-419-36-39 US-09-419-36-39 US-09-419-36-39 US-09-419-36-39 US-09-419-36-39 US-09-419-453-7 US-09-419-453-7 US-09-419-453-7 US-09-419-453-7 US-09-419-453-7 US-09-419-453-7 US-09-419-453-7 US-09-419-453-7 US-09-419-453-7 US-09-53-41-33 US-09-53-41-31
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INFORMATION: Xaa = Ala, Cys, Asp, Phe, Gly, His, Ile, Leu, Asn, Pro, Arg, Ser, Thr, Val, Ty
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Sequence 61, Application US/09538092;
Patent No. 675314
GENERAL INFORMATION:
APPLICANT: Glot, Loid
TITLE OF INVENTION:
PILE REPRENCE: 1596-542
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 06/127,352
PRIOR PILING DATE: 2000-03-29;
PRIOR PLILNG DATE: 2000-03-29;
PRIOR PLILNG DATE: 2000-03-01
PRIOR PLILNG DATE: 2000-02-01
PRIOR PLILNG DATE: 2000-02-01
PRIOR PLILNG DATE: 2000-02-01
PRIOR PLILNG DATE: 2000-02-01
PRIOR PLING DATE: 2000-02-01
PRIOR SEQ ID NOS: 1387
SOFTWARE: CuraPatSeqFormatter Version 0.9
SOFTWARE: CuraPatSeqFormatter Version 0.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 ESDSVQPVPRFRQELFRAMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAELG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MDPKIGRMAASILAVILILILIERGMFSSPSPPPALLEKVFQYIDIHQDEFVQTLKEWVAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MDPKLGRMAASLLAV-LLLLLERGMFSSPPPPALLEKVFQYIDLHQDEFVQTLKEWVAI
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                                                                                                                                                                                                                                                                                                        Cys, Asp, Glu, Phe, Gly, Leu, Val, Trp, Tyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 148;
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; OTHER INFORMATION: Polypeptide Accession Number YBR281C
US-09-538-092-61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 607.5; DB 2;
Pred. No. 1.7e-51;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Xaa = Lys, Asn, Arg, Ser, Thr
US-09-621-976-3957
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 3957
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                                                                                                                                                                                                                                                                                                                                                                                                                                               = Cys, Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 23.2%;
Best Local Similarity 96.9%;
Matches 124; Conservative
                                                                                                                                                                                                                                                                                   LOCATION: 93
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Xaa
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                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                          -27...-1
UNSURE
                                                                                                                                                                                                                   NAME/KEY: SIGNAL
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US-09-538-092-61
                                                                                                                                                                                                                                          LOCATION:
NAME/KEY:
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GENERAL INFORMATION:
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GENERAL INFORMATION:
FILLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REFERENCE: 107196-132
CURRENT APPLICATION NUMBER: US 60/074,725
FILLE REPERENCE: 1998-02-13
FRIOR PAPLICATION NUMBER: US 60/096,409
FRIOR PAPLICATION NUMBER: US 60/096,409
FRIOR PELING DATE: 1998-08-13
FRIOR PELING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 14755
LENGTH: 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: UNSURE
1 LOCATION: (488)
2 LOCATION: (488)
1 CARE INFORMATION: Identity of amino acid sequences at the above locations are unknot US-09-248-796A-14755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 YDKEKEILYGRGSTDDKGPVVGMLAVIEAHNKLGWELPVNLVVCFEGMEESGSLGLDELV 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               331 FDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFSIRLVPHANVSAVEKQV 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 HDNKKDILKHRMRFPSLSLHGIEGAFSGAGAKTVIPAKVVGKFSIRTVPDIESKKLDDLV 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|: || || || || || || 377 FQHITSEFKKLNSPNKFKVELIHDGNYWVSDPFNDSFTAAAKATQDVWNVVPDFTREGGS 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 EVDGK--LYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELV 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 EKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILH 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEBEINTYKAIHLDLEEYRNSSRVEKFL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94 SVDMGPQQLP-DGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQPADRGDGWLTDPYVLT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 LEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELFRMMAVAADTLQRLG-ARVA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         391 TRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGST
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Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Unmas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
                                                    Sequence 14755, Application US/09248796A Patent No. 6747137
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Candida albicans
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US-09-621-976-3957
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Sequence 4829 Application US/09583110

j Sequence 4829 Application US/09583110

j Return No. 6699703

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al.

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus

FILE REFERENCE: PATHOD-07A

CURRENT PILING DATE: 1090-05-26

PRIOR PILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1998-05-12

PRIOR FILING DATE: 1997-07-02

NUMBER OF SEQ ID NOS: 5322

SEQ ID NO 4829
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                                                                                                                                                                                                                                                                                                                          ECEBNIGFRPQGYEASYSPEESALR-----PTVEINGISGGYTGPGFKTVIPYRATAYLS 363
                                                                                                                                                                                                                                                                                                                                                                             375 IRLVPHMNVSAVEKQVTRHLED-----VFSK-----RNSSNKMVVSMTLGLHPW 418
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                                                                                                                                                                                                                                                                                                                                                                                                               364 CRLVPNODPDKAAHQVIHHLKQQVPSSLKFSYEILPGGSRGWRSSANLPIVKVLQEIYSD 423
                                                                                                                                                                      103 PDGQSLPIPPVILAELGSDPTKGTVCPYGHLDVQPADRGDGWLTDPYVLTEVDGKLYGRG
                                                                                                                                                  MEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRD
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                                   ---VDHVNKI-----PDVELWETPGH-----PPIIYASYKSEDPLSPTLMLYNHYDVQP
                                                                           ADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEG
79 AVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILABLGS-DPTKGTVCFYGHLDVQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQNEKINRWNYIEGTKLFAAFFLEMAQL 506
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US-09-583-110-4829
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                                                                                                                                                                                                                                                   71 ROELFRMMAVAADTLQRLGARVASVDMGPQQL-----PDGQSLPIP----PVILAELGS 120
                                                                                                  WINAVSAFRALEQDLFVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWI 232
                                                                                                                                                                                                                                                                                                      233 SQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILV 292
                                                                                                                                                                                                                                                                                                                                                                               PGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGI 352
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 SLLAVLLLLLERGMFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRF 70
                                                                                                                                                                                                                                                                                                                            620 DQEHPCLNYGLRGVINAQIKVWSDKPDGHSGLNGGVYDEPMVNLVKIVSKLQNEQNEIMI
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                       Indels
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APPLICANT: Kalman, Sue
APPLICANT: Davis, Ronald
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 17.2%; Score 451.5; DB 2; Best Local Similarity 27.0%; Pred. No. 2.6e-35; Matches 137; Conservative 91; Mismatches 203;
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CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR FILING DATE: 1999-04-08
NUMBER OF SEQ ID NOS: 1074
SOFTWARE: PSECSEQ for Windows Version 3.0
SEQ ID NO 981
LENGTH: 495
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APPLICANT: Stephens, Richard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Chlamydia pneumoniae
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US-09-438-185A-981
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US-09-438-185A-981
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Sequence 14559, Application US/09248796A
| Patent No. 6747137
| Patent INCOMPATION:
| APPLICANT: Keith Weinstock et al | TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANTING TO INVENTION: NUCLEIC ACID AND THERAPEUTICS | TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS | FILE REFERENCE: 107196.132 | CURRENT APPLICATION NUMBER: US/09/248,796A
                          Sequence 15643, Application US/09902540

Sequence 15643, Application US/09902540

Patent No. 6833447

GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.

APPLICANT: Goldman, Roger C.

APPLICANT: Miegand, Roger C.

TITLE OF INVENTION: Myxococcue xanthus Genome Sequences and Uses Thereof

TITLE OF INVENTION: Myxococcue xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849) B

CURRENT APPLICATION NUMBER: US/09/902,540

CURRENT FILING DATE: 2001-07-10

PRIOR PILING DATE: 2000-07-10

PRIOR PILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825

SEQ ID NO 15643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 DRGFENV---QLLEIBGTHPYVYGSVLKAPGKPTLLLYAHHDVQPAGDBAAWKSPPREPV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 MADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSRV---EKF 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 134; Conservative
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US-09-248-796A-14559
                             US-09-902-540-15643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Griffals, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: and treatment of infection
TITLE OF INVENTION: US. 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
SEQ ID NOS: 6849
SEQ ID NOS: 6849
LENGTH: 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10,
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                                                                                                                                                                                                                                      401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 ADRGDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 MEEAGSVALEELVEKEKORFFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRD 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 KOMHSGVIGGIAYNTNRALSEILSSLHHPDNSIAIEGFYDDLALPSDSDRPDLPKSDTLR 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
                               DIKEBILMHLWRY---PSLSIHGIEGARDEPGTKTVIPGRVIGKFSIRLVPHMNVSAVEK 388
                                                                                                                                                                                                                                                                                                         QVTRHLEDVFSKRNSSNKMVVSMTLG-----LHPWIANIDDTQ---YLAAKRAIRTV 437
YIVISDNIMISQRKPA----ITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLV 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 MFSSPSPPPALLEKVFQYIDLHQDEFVQTLKEWVAI----ESDSVQPVPRFRQELFRMM 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           189 EEESGSLALFTWLEKKKEAL--RADYLLIVDGGFLSEKHPYVSIGARGIVSMKISLEEGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ODFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEV-VPLTEEEINTYKAIHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 ECEENLGFRPQGYEASYSPEESALR----PTVEINGISGGYTGPGFKTVIPYRATAYLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       317 LEEYRNSSRVEKF--LFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGKFS
                                                                                                                                                                                                                                                                                                                                           347 KIRKQLD-----KNGFDKVELYYTLGEMSYRSDMSAPALLNVIELAKKFYPQGVSVLPTT
                                                                                                    278 ALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEY--RNSSRVEKF---LF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                             402 AGTGPMHTVFDALEVP-------WVAFGLGNANSRDHGGDENVRIADY
                                                                                                                                                                                                                                                                                                                                                                                                                438 FGTEP-DMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 16.3%; Score 428; DB 2; Length 39 Best Local Similarity 29.9%; Pred. No. 3.6e-33; Matches 114; Conservative 73; Mismatches 158; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1054, Application US/09198452A Patent No. 6559294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            375 IRLVPHMNVSAVEKQVTRHLE 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129
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ORGANISM:
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87 RLGARVASVDMGP-----QQLPDGQSLPIPPVILAELGSDPTKGTVCFYGHLDVQPADR 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 -LETYGQRNPEEVSRIYGLELPLLQEERMAFLKRFFFEPALNIEGIQSGYQGQGVKTIVP 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 GDGWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEE 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             201 AGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPA----ITYGTRGNSYFMVEVKC 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 DLEEY--RNSSRVEKF----LFDTKEEILMHLWRY---PSLSIHGIEGAFDEPGTKTVIP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 RLDSRKSQITLGEIFKRVGAEVEIDESYTAPFVWAHFKSSRPDAKTLIFYNHYDTVPADG
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184 ADVDIHS-SYGGVVESAPWYLLQALQSLRAADGRILVEGLYEEVHEPNEREMAL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDQDFHSGTFGGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
14.0%; Score 367; DB 2; Length 304;
Best Local Similarity 32.7%; Pred. No. 2.3e-27;
Matches 101; Conservative 49; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.0%; Score 261; DB 2; Length 103; 51.0%; Pred. No. 1e-17; cive 18; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Pro
FILE REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 4417
LENGTH: 103
                                                                                                                                                                                                                                                                                                                       ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (B) LÖCATION 1...304
SEQUENCE DESCRIPTION: SEQ ID NO: 3644:
    REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTT
TELECOMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4417, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
                                                                                              TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3644:
SEQUENCE CHARACTERISTICS:
LENGTH: 304 amino acid
TYPE: amino acid
                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Conservative
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CRGANISM: Homo sapiens
US-09-621-976-4417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 51; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSVALBELVEKEKDRF------FSGVDYIVISDNLWISQRKPAITYGTRGNSYFM 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               251 VEVKCRDQDFHSGTFGGILHEPMADLVALLGSLVDS-SGHILVPGIYDEVVPLTEERINT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95 VDMGPQQLPDGQSLPIP---PVILAEL-GSDPTKGT-----VCFYGHLDVQPADRGDG 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --WLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEA 201
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Sequence 3644, Application US/09107433
Batent No. 6800744
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                             44 LHQDEFVQTLKEWVAIESDSVQP-----VPRFRQELFRMMAVAADTLQRLGARVAS
                                                                                                                                                                                                                                                                                                                                                                                                                        34 LSNDDMLIMLQKYVAPKTISKNPQLYLEESRHCAQFLCKLFN----------
                                                                                                                                                                                                                                                                                                                                             75;
                                                                                                                                                                                                                                                                                         Query Match 15.1%; Score 395.5; DB 2; Length 345; Best Local Similarity 30.1%; Pred. No. 4.6e-30; Matches 104; Conservative 58; Mismatches 109; Indels 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 YDTIAQYLGIKVY------TLATKWREPSLTIHKIQ 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YKAI -- HLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIE 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/107,433 FILING DATE: 30-Jun-1998 PRIOR APPLICATION DATA:
; CURRENT FILING DATE: 1999-02-12;
; PRIOR APPLICATION NUMBER: US 60/074,725;
; PRIOR FILING DATE: 1998-02-13;
; PRIOR APPLICATION NUMBER: US 60/096,409;
; PRIOR FILING DATE: 1998-08-13;
; NUMBER OF SEQ ID NOS: 28208;
; SEQ ID NO 14559;
; LENCTH: 345
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PILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ariniello, Pamela Deneke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 100 Beaver Street
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STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                        ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                             ; ORGANISM: Candid:
US-09-248-796A-14559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-107-433-3644
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APPLICANT: FORGET, BATKARS
APPLICANT: FORGET, HATKARS
APPLICANT: FORGET, HATKARS
APPLICANT: GAIGAT, CANAT
TILE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
TILE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION
TILE OF INVENTION: OF DATE: 1200-06-23
TILE OF INVENTION OF DATE: 1200-06-23
FRICK APPLICATION NUMBER: US 6/141031
PRIOR PILLING DATE: 1309-06-25
PRIOR PELLING DATE: 1309-07-06
PRIOR FILLNG DATE: 1309-07-06
PRIOR FILLNG DATE: 1309-07-06
PRIOR PILLNG DATE: 1309-07-14
PRIOR PILLNG DATE: 1309-07-14
PRIOR PILLNG DATE: 1309-07-14
PRIOR PELLNG DATE: 1309-07-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AALTTLFKYIDENQDRYIKKUAKWVAIQ--SVSAWPEKRGEIRRMMEVAAADVKQLGGSV 59
                                                                                                                                                                                                                                                                                                                      Query Match 9.5%; Score 248; DB 2; Length 98; Best Local Similarity 49.5%; Pred. No. 1.8e-16; Matches 49; Conservative 18; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93 ASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 ELVDIGKQKLPDGSXIPLPPILXGRLGSDPQKKTVCIYG 98
                        PEATURE:
NAME/KEY: UNSURE
LOCATION: 74
OTHER INFORMATION: Xaa= * or Glu or Lys or Gln
                                                                                                                                                                                                                                ) OTHER INFORMATION; Xaa=His or lle or Leu or Asn
US-09-513-999C-5702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 192, Application US/09602777A; Patent No. 6831165; GENERAL INFORMATION: APPLICATT: Pompejus, Markus
ORGANISM: Homo sapiens
                                                                                                                                                                         NAME/KEY: UNSURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
US-09-602-777A-192
                                                                                                                                                                                                    LOCATION: 82
                                                                                                                                                FEATURE:
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Batent No. 6783961

GENERAL INFORMATION:
APPLICANT: Duclert, A.
APPLICANT: Duclert, A.
TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961

TILLE REFERENCE: 59. US2. REG.
CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT APPLICATION NUMBER: US 60/122,487

PRIOR APPLICATION NUMBER: US 60/122,487

PRIOR PILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33 ALLEKVPQYIDLHQDEFVQTLKEWVAIESDSVQPVPRPRQELPRWMAVAADTLQRLGARV 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 AALTTLFKYIDENQDRYIKKCLAKWVAIQ--SVSAWPEKRGEIRRAMBVAAADVKQLGGSV 59
33 ALLEKVFQYIDLHQDEFVQTLKEWVAIESDSVQPVPRFRQELFRMMAVAADTLQRLGARV 92
                                                                                                                                                                                                                                                                                                                                                                                                                               2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 9.5%; Score 248; DB 2; Length 98; Best Local Similarity 49.5%; Pred. No. 1.8e-16; Matches 49; Conservative 18; Mismatches 30; Indels
                                                                                                                    93 ASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYGH 132
                                                                                                                                                   60 ELVDIGKQKLPDGSEIPLPPILLGRLGSDPQKKTVCIYGH 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93 ASVDMGPQQLPDGQSLPIPPVILAELGSDPTKGTVCFYG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 ELVDIGKQKLPDGSXIPLPPILXGRLGSDPQKKTVCIYG 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or Glu or Lys or Gln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Xaa=His or Ile or Leu or Asn
US-09-513-999C-5701
                                                                                                                                                                                                                                                                                                                      Sequence 5701, Application US/09513999C Patent No. 6783961
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 74
OTHER INFORMATION: Xaa= *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: UNSURE
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US-09-513-999C-5702
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LENGTH: 98
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PRIOR APPLICATION NUMBER: DE 19932128.0
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR PLING DATE: 1999-07-19
PRIOR PLING DATE: 1999-07-19
PRIOR PLING DATE: 1999-07-19
PRIOR PLING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933005.0
PRIOR PLING DATE: 1999-07-14
PRIOR PLING DATE: 1999-08-31
PRIOR PLING DATE: 1999-09-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 34.9
Matches 67; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-602-777A-194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 LPDGQSLPIPPVILAELGSDPTKGT------VCFYGHLDVQPADRGDGWLTDPYVLT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         153 EVDG----KLYGRGATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEE 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 ERDAGHGTRWYGRGAADCKGNLVWHLAALRAVBA-SGDTTLNLTYVVBGSEBMGGGALSA 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pompejus, Markus
APPLICANT: Pompejus, Markus
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Leder, OGENERATER, GENERALIANT: Haberhauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: LOOPORTASIS AND ADAPTATION
FILE REFERENCE: BEI - 128CP
CURRENT APPLICATION NUMBER: US 60/141031
PRIOR PLILING DATE: 1999-06-23
PRIOR PLILING DATE: 1999-06-25
PRIOR PLILING DATE: 1999-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVEKEKDRPFSGVDYIVISDNLWISQRKPAITYGTRGNSYFMVEVKCRDQDFHSGTFGGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 9.2%; Score 242.5; DB 2; Best Local Similarity 29.7%; Pred. No. 3.2e-15; Matches 79; Conservative 37; Mismatches 113;
                          PRIOR PLING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933005.0
PRIOR PILING DATE: 1999-07-14
PRIOR PLILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: DE 19933006.9
PRIOR PILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR APPLICATION NUMBER: DE 19941379.7
PRIOR APPLICATION NUMBER: DE 19941390.8
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PLING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19942088.2
PRIOR PLING DATE: 1999-09-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 LHEPMADLVALLGSLVDSSGHILVPG 294
        DE 19933003.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT; ORGANISM: Corynebacterium glutamicum US-09-602-777A-192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 194, Application US/09602777A
Patent No. 6831165
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LENGTH: 267
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163 ATDNKGPVLAWINAVSAFRALEQDLPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVD 222
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                                                                                                                                                                                                                                                                                                                                                                          31 AEDGITINFIGIRKGSEGAPKVLLYSHFDVVPSGPLDLWDINPFELTERDAGHGTRWYGRG 90
                                                                                                                                                                                                                                                          116 AELGSDPTKGT-----KLYGRGLDVQPADRGDGWLTDPYVLTEVDG----KLYGRG
                                                            Gaps
                                                            16;
8.9%; Score 233; DB 2; Length 231; 34.9%; Pred. No. 2.1e-14; Live 27; Mismatches 82; Indels
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Sequence 219, App Sequence 104, App Sequence 1054, App Sequence 2902, App Sequence 2902, App Sequence 910, App Sequence 91, App Sequence 32013, A Sequence 52113, App Sequence 52113, App Sequence 52113, App Sequence 22, Appl Sequence 21102, App Sequence 3112, App Sequence 3113, App Sequence 3114, App Sequence 3144, App Sequence 3144, App Sequence 3144, App Sequence 31444, App Sequence 31444, App Sequence 31444, App Sequence 314
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US-10-474-776-219

US-10-4772-928-104

US-10-282-1054

US-10-501-282-2902

US-10-501-282-2902

US-10-11410-910

US-10-11410-9
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139.5
                                                        1397, 4p
103, App
25548, A
46235, A
78, Appl
1427, Ap
16236, A
48298, A
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1139, App
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242, App
371, App
54, App
674, App
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(without alignments)
1260.949 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Biocceleration Ltd.
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US-10-036-160-57
US-10-275-107-68
US-10-884-091-56
US-09-731-872-242
US-09-948-733-139
US-09-948-733-139
US-09-948-73-139
US-09-948-73-139
US-09-948-73-139
US-09-949-836-2427
US-09-949-836-2427
US-09-991-391-2
US-09-791-393-2
US-09-791-393-2
US-09-791-377-674
US-10-26-381-18
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US-10-156-761-10612
US-10-282-122A-48298
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Maximum Match 100%
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                             GenCore version
Copyright (c) 1993 - 2006
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